Amendments to the Specification:

Please replace the paragraph beginning at page 8, line 18, with the following redlined paragraph.

Figure 3 depicts amino acid sequence of the ABCG4 transporter molecule corresponding to amino acids 1 to 646 which is represented by SEQ ID NO: 2. Sequences corresponding to transmembrane helices (SEQ ID NOs:18-23) are underlined; Walker A (SEQ ID NO:9), ABC signature motif (C signature) (SEQ ID NO:10), and Walker B (SEQ ID NO:11) are shown in shaded boxes.

Please replace the paragraph beginning at page 8, line 20, with the following redlined paragraph.

Figure 4 depicts the multiple sequence alignment of the members of the ABCG subfamily ~~(SEQ ID NOs:4-7)~~: ABCG1 (SEQ ID NO:4); ABCG4 (SEQ ID NO:2); ABCG2 (SEQ ID NO:5); ABCG5 (SEQ ID NO: 6); ABCG8 (SEQ ID NO:7).

Please replace the paragraph beginning at page 16, line 21, with the following redlined paragraph.

In still another preferred embodiment, an isolated nucleic acid molecule of the present invention comprises a nucleotide sequence which is at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or more identical to the entire length of the nucleotide sequence shown in SEQ ID NOs: 1, 3, or 12, or a portion of any of these nucleotide sequences. The identity algorithms and settings that may be used includes computer programs which employ the Smith-Waterman algorithm, such as the MPSRCH program (Oxford Molecular), using an affine gap search with the

following parameters: a gap open penalty of 12 and a gap extension penalty of 1. Preferably, GCG PileUp program (Genetics Computer Group, Madison, Wisconsin) (Gapweight: 4, Gaplength weight: 1) is used for sequence alignment. Alternatively, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at Internet<URL:http://www.gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6.

Please replace the paragraph beginning at page 29, line 26, with the following redlined paragraph.

A comparison of sequences and determination of percent identity and/or similarity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using standard art recognized comparison software using standard parameter settings. For example, the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at Internet<URL:http://www.gcg.com) can be employed using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

Please replace the paragraph beginning at page 30, line 10, with the following redlined paragraph.

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for example, identify

other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to ABCG4 transporter nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to ABCG4 transporter protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used. See Internet<URL:http://www.ncbi.nlm.nih.gov.

Please replace the paragraph beginning at page 62, line 13, with the following redlined paragraph.

The cell-free assays of the present invention are amenable to use of both soluble and/or membrane-bound forms of isolated proteins (*e.g.*, ABCG4 transporter proteins or biologically active portions thereof). In the case of cell-free assays in which a membrane-bound form of an isolated protein is used it may be desirable to utilize a solubilizing agent such that the membrane-bound form of the isolated protein is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100 (octyl phenol ethoxylate), Triton® X-114 (octylphenol-polyethylene glycol ether), Thesit® (dodecylpoly(ethylene glycol ether)$_n$ (n = 9–10)), Isotridecypoly(ethylene glycol ether)$_n$, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane sulfonate (CHAPS), 3-[(3-cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-dodecyl=N,N-dimethyl-3-ammonio-1-propane sulfonate.

Please replace the paragraph beginning at page 88, line 6, with the following redlined paragraph.

Bioinformatics analysis of the genomic sequence AC000384 reveals a putative open reading frame (ORF) in which the 3' end matched the EST AL137563. Oligonucleotides were generated using the above-mentioned nucleotide sequences and used to produce a complementary DNA (cDNA) fragment. It is a 3455 base pair (bp) fragment obtained by reverse transcriptase polymerase chain reaction (RTPCR) from human brain total RNA using oligonucleotides P1 and P2 (defined below). The cDNA sequence was obtained using a LICOR automated DNA sequencing engine. The sequencing data identified a 1941 nucleotide fragment that contains the complete open reading frame of the invention. By comparison to the nucleotide and amino acid sequence data banks, the deduced amino acid sequence of the invention reveals a unique human protein. The closest protein homologs are ABCG1, ABCG2, ABCG5, ABCG8 (80%, 47%, 44% and 43% similarity, respectively), members of the ATP-binding cassette (ABC) transporter superfamily (gene nomenclature approved by the Human Genome Organization (*see* Internet<URL:http://www.gene.ucl.ac.uk/nomenclature/)) (Table 1). The percentage of nucleotide identity between the isolated ABCG4 and its closest homologs according to Pairwise Global Aligment (MacVector 7.0) is shown in Table 2. The ABC transporter superfamily is divided into several groups in which proteins share common structural features. Therefore human ABCG4 transporter is a new ABC transporter that belongs to the G group.

Please replace the paragraph beginning at page 96, line 7, with the following redlined paragraph.

Bioinformatics analysis of the genomic sequence AC000384 reveals a putative open reading frame (ORF) in which the 3' end matched the EST AL137563. Oligonucleotides were generated using the above-mentioned nucleotide sequences and used to produce a complementary DNA (cDNA) fragment. It is a 2687 base pair (bp) fragment (SEQ ID NO:12:

Figure 10) obtained by reverse transcriptase polymerase chain reaction (RTPCR) from human brain total RNA using oligonucleotides P3 and P4 (SEQ ID NOs:16 and 17, respectively, defined below). The cDNA sequence was obtained using a LICOR automated DNA sequencing engine. The sequencing data identified a 1941 nucleotide fragment that contains the complete open reading frame of the invention. By comparison to the nucleotide and amino acid sequence data banks, the deduced amino acid sequence of the invention reveals a unique human protein. The closest protein homologs are ABCG1, ABCG2, ABCG5, ABCG8 (80%, 47%, 44% and 43% similarity, respectively), members of the ATP-binding cassette (ABC) transporter superfamily (gene nomenclature approved by the Human Genome Organization (*see* Internet<URL:http://www.gene.ucl.ac.uk/nomenclature/)) (Table 3). The percentage of nucleotide identity between the isolated ABCG4 and its closest homologs according to Pairwise Global Aligment (MacVector 7.0) is shown in Table 4. The ABC transporter superfamily is divided into several groups in which proteins share common structural features. Therefore human ABCG4 transporter is a new ABC transporter that belongs to the G group.

Please delete the section of the Application entitled "Sequence Listing" immediately after the section of the specification entitled "Abstract of the Disclosure" on page 105 and insert the enclosed Sequence Listing therefor.